

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
Carroll, Joseph M.

<120> 23565, A NOVEL HUMAN ZINC
CARBOXYPEPTIDASE FAMILY MEMBER AND USES THEREOF

<130> 10448-142001

<150> 60/269,440

<151> 2001-02-16

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1687

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (160)...(1467)

<221> misc_feature

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cccaaggaaa	gcccctgaag	ctcaccagga	ggaagaagc	atg cag ggc	act cct	174
				Met Gln Gly	Thr Pro	
				1	5	

gga ggc ggg	acg cgc cct	ggg cca tcc	ccc gtg	gac agg cgg	acg ctc	222
Gly Gly Gly	Thr Arg Pro	Gly Pro Ser	Pro Val	Asp Arg Arg	Thr Leu	
10	15	20				

ctg gtc ttc	agc ttt atc	ctg gca	gct ttg	ggc caa	atg aat ttc	270
Leu Val Phe	Ser Phe Ile	Leu Ala	Ala Leu	Gly Gln	Met Asn Phe	
25	30	35				

aca ggg gac	cag gtt ctt	cga gtc	ctg gcc	aaa gat	gag aag cag ctt	318
Thr Gly Asp	Gln Val Leu	Arg Val Leu	Ala Lys	Asp Glu Lys	Gln Leu	
40	45	50				

tca ctt ctc	ggg gat ctg	gag ggc	ctg aaa ccc	cag aag	gtg gac ttc	366
Ser Leu Leu	Gly Asp Leu	Glu Gly Leu	Lys Pro	Gln Lys	Val Asp Phe	
55	60	65				

tgg cgt ggc	cca gcc agg	ccc agc ctc	cct gtg	gat atg	aga gtt cct	414
Trp Arg Gly	Pro Ala Arg	Pro Ser Leu	Pro Val	Asp Met	Arg Val Pro	

70

75

80

85

ttc tcc gaa ctg aaa gac atc aaa gct tat ctg gag tct cat gga ctt 462
 Phe Ser Glu Leu Lys Asp Ile Lys Ala Tyr Leu Glu Ser His Gly Leu
 90 95 100

gct tac agc atc atg ata aag gac atc cag gtg ctg ctg gat gag gaa 510
 Ala Tyr Ser Ile Met Ile Lys Asp Ile Gln Val Leu Leu Asp Glu Glu
 105 110 115

aga cag gcc atg gcg aaa tcc cgc cggt ctg gag cgc agc acc aac agc 558
 Arg Gln Ala Met Ala Lys Ser Arg Arg Leu Glu Arg Ser Thr Asn Ser
 120 125 130

ttc agt tac tca tca tac cac acc ctg gag gag ata tat agc tgg att 606
 Phe Ser Tyr Ser Ser Tyr His Thr Leu Glu Glu Ile Tyr Ser Trp Ile
 135 140 145

gac aac ttt gta atg gag cat tcc gat att gtc tca aaa att cag att 654
 Asp Asn Phe Val Met Glu His Ser Asp Ile Val Ser Lys Ile Gln Ile
 150 155 160 165

ggc aac agc ttt gaa aac cag tcc att ctt gtc ctg aag ttc agc act 702
 Gly Asn Ser Phe Glu Asn Gln Ser Ile Leu Val Leu Lys Phe Ser Thr
 170 175 180

gga ggt tct cgg cac cca gcc atc tgg atc gac act gga att cac tcc 750
 Gly Gly Ser Arg His Pro Ala Ile Trp Ile Asp Thr Gly Ile His Ser
 185 190 195

cggtt gat acc cat gcc acc ggc atc tgg act gcc aat aag att 798
 Arg Glu Trp Ile Thr His Ala Thr Gly Ile Trp Thr Ala Asn Lys Ile
 200 205 210

gtc agt gat tat ggc aaa gac cgt gtc ctg aca gac ata ctg aat gcc 846
 Val Ser Asp Tyr Gly Lys Asp Arg Val Leu Thr Asp Ile Leu Asn Ala
 215 220 225

atg gac atc ttc ata gag ctc gtc aca aac cct gat ggg ttt gct ttt 894
 Met Asp Ile Phe Ile Glu Leu Val Thr Asn Pro Asp Gly Phe Ala Phe
 230 235 240 245

acc cac agc atg aac cgc tta tgg cgg aag aac aag tcc atc aga cct 942
 Thr His Ser Met Asn Arg Leu Trp Arg Lys Asn Lys Ser Ile Arg Pro
 250 255 260

gga atc ttc tgc atc ggc gtg gat ctc aac agg aac tgg aag tcg ggt 990
 Gly Ile Phe Cys Ile Gly Val Asp Leu Asn Arg Asn Trp Lys Ser Gly
 265 270 275

ttt gga gga aat ggt tct aac agc aac ccc tgc tca gaa act tat cac 1038
 Phe Gly Gly Asn Gly Ser Asn Ser Asn Pro Cys Ser Glu Thr Tyr His
 280 285 290

ggg ccc tcc cct cag tcg gag tcg gag gtg gct gcc ata gtg aac ttc 1086
 Gly Pro Ser Pro Gln Ser Glu Ser Glu Val Ala Ala Ile Val Asn Phe
 295 300 305

atc aca gcc cat ggc aac ttc aag gct ctg atc tcc atc cac agc tac Ile Thr Ala His Gly Asn Phe Lys Ala Leu Ile Ser Ile His Ser Tyr 310 315 320 325	1134
tct cag atg ctt atg tac cct tac ggc cga ttg ctg gag ccc gtt tca Ser Gln Met Leu Met Tyr Pro Tyr Gly Arg Leu Leu Glu Pro Val Ser 330 335 340	1182
aat cag agg gag ttg tac gat ctt gcc aag gat gcg gtg gag gcc ttg Asn Gln Arg Glu Leu Tyr Asp Leu Ala Lys Asp Ala Val Glu Ala Leu 345 350 355	1230
tat aag gtc cat ggg atc gag tac att ttt ggc agc atc agc acc acc Tyr Lys Val His Gly Ile Glu Tyr Ile Phe Gly Ser Ile Ser Thr Thr 360 365 370	1278
ctc tat gtg gcc agt ggg atc acc gtc gac tgg gcc tat gac agt ggc Leu Tyr Val Ala Ser Gly Ile Thr Val Asp Trp Ala Tyr Asp Ser Gly 375 380 385	1326
atc aag tac gcc ttc agc ttt gag ctc cgg gac act ggg cag tat ggc Ile Lys Tyr Ala Phe Ser Phe Glu Leu Arg Asp Thr Gly Gln Tyr Gly 390 395 400 405	1374
ttc ctg ctg ccg gcc aca cag atc atc ccc acg gcc cag gag acg tgg Phe Leu Leu Pro Ala Thr Gln Ile Ile Pro Thr Ala Gln Glu Thr Trp 410 415 420	1422
atg gcg ctt cgg acc atc atg gag cac acc ctg aat cac ccc tac Met Ala Leu Arg Thr Ile Met Glu His Thr Leu Asn His Pro Tyr 425 430 435	1467
tagcagcacg actgagggca ggaggctcca tccttctccc caaggtctgt ggctcctccc gaaacccaag ttatgcattcc ccatccccat gccctcatcc cgacctctta gaaaataaat acaagttga acaggcaaaa aaaaaaaaaa aaaaaaaaaat tggcgccgc aagcttattc ctttaagtga gggtaattt tagcttggca ctggccgncc	1527 1587 1647 1687
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Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Leu 20 25 30	
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys 35 40 45	
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro 50 55 60	
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val 65 70 75 80	
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp Ile Lys Ala Tyr Leu 85 90 95	
Glu Ser His Gly Leu Ala Tyr Ser Ile Met Ile Lys Asp Ile Gln Val	

100	105	110
Leu Leu Asp Glu Glu Arg Gln Ala Met Ala Lys Ser Arg Arg	Leu Glu	
115	120	125
Arg Ser Thr Asn Ser Phe Ser Tyr Ser Ser Tyr His Thr Leu	Glu Glu	
130	135	140
Ile Tyr Ser Trp Ile Asp Asn Phe Val Met Glu His Ser Asp Ile	Val	
145	150	155
Ser Lys Ile Gln Ile Gly Asn Ser Phe Glu Asn Gln Ser Ile	Leu Val	
165	170	175
Leu Lys Phe Ser Thr Gly Gly Ser Arg His Pro Ala Ile Trp	Ile Asp	
180	185	190
Thr Gly Ile His Ser Arg Glu Trp Ile Thr His Ala Thr Gly	Ile Trp	
195	200	205
Thr Ala Asn Lys Ile Val Ser Asp Tyr Gly Lys Asp Arg Val	Leu Thr	
210	215	220
Asp Ile Leu Asn Ala Met Asp Ile Phe Ile Glu Leu Val	Thr Asn Pro	
225	230	235
Asp Gly Phe Ala Phe Thr His Ser Met Asn Arg Leu Trp Arg	Lys Asn	
245	250	255
Lys Ser Ile Arg Pro Gly Ile Phe Cys Ile Gly Val Asp Leu	Asn Arg	
260	265	270
Asn Trp Lys Ser Gly Phe Gly Gly Asn Gly Ser Asn Ser Asn	Pro Cys	
275	280	285
Ser Glu Thr Tyr His Gly Pro Ser Pro Gln Ser Glu Ser Glu	Val Ala	
290	295	300
Ala Ile Val Asn Phe Ile Thr Ala His Gly Asn Phe Lys Ala	Leu Ile	
305	310	315
Ser Ile His Ser Tyr Ser Gln Met Leu Met Tyr Pro Tyr Gly	Arg Leu	
325	330	335
Leu Glu Pro Val Ser Asn Gln Arg Glu Leu Tyr Asp Leu Ala	Lys Asp	
340	345	350
Ala Val Glu Ala Leu Tyr Lys Val His Gly Ile Glu Tyr Ile	Phe Gly	
355	360	365
Ser Ile Ser Thr Thr Leu Tyr Val Ala Ser Gly Ile Thr Val	Asp Trp	
370	375	380
Ala Tyr Asp Ser Gly Ile Lys Tyr Ala Phe Ser Phe Glu Leu	Arg Asp	
385	390	395
Thr Gly Gln Tyr Gly Phe Leu Leu Pro Ala Thr Gln Ile Ile	Pro Thr	
405	410	415
Ala Gln Glu Thr Trp Met Ala Leu Arg Thr Ile Met Glu His	Thr Leu	
420	425	430
Asn His Pro Tyr		
435		

<210> 3

<211> 1311

<212> DNA

<213> Homo sapiens

<400> 3

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cagg	tttc	gagt	cctgg	caaagatgag	aagcagctt	cacttctgg	180
gcctgaaac	ccc	agaaggt	ggacttctgg	cgtggccag	ccaggcccag	cctccctgtg	240
gatatgagag	ttc	tttctc	cgaactgaaa	gacatcaaag	cttatctgga	gtctcatgga	300
tttg	ttt	taca	gcatcatgat	aaaggacatc	caggtgctgc	tggatgagga	360
atggc	aaat	cccgccggct	ggagcgcagc	accaacagct	tcagttactc	atcataaccac	420

accctggagg	agatataatag	ctggattgac	aactttgtaa	tggagcattc	cgatattgtc	480
tcaaaaattc	agattggcaa	cagcttgaa	aaccagtcca	ttcttgcct	gaagttcagc	540
actggagggt	ctcggcaccc	agccatctgg	atcgacactg	gaattcactc	ccgggagtg	600
atcacccatg	ccaccggcat	ctgactgccc	aataagattg	tcaagtgatta	tggcaaagac	660
cgtgtcctga	cagacatact	gaatgccatg	gacatctca	tagagctcg	cacaaccct	720
gatgggtttg	cttttaccca	cagcatgaac	cgcttatggc	ggaagaacaa	gtccatcaga	780
cctgaatct	tctgcatcg	cgtggatctc	aacaggaact	ggaagtgcgg	ttttggagga	840
aatgttcta	acagcaaccc	ctgctcagaa	acttacacg	ggccctcccc	tcaagtccgg	900
tcggaggtgg	ctgccatagt	gaacttcatac	acagccatg	gcaacttcaa	ggctctgatc	960
tccatccaca	gctactctca	gatgctttag	tacccttacg	gcccattgtc	ggagcccg	1020
tcaaatacaga	gggagttgt	cgatcttgcc	aaggatgcgg	tggaggcctt	gtataagg	1080
catgggatcg	agtacat	tggcagcatac	agcaccaccc	tctatgtggc	cagtggatc	1140
accgtcgact	gggcctatga	cagtggcatac	aagtacgcct	tcaagttga	gctccggac	1200
actgggcagt	atggcttcct	gctgccggcc	acacagatca	tccccacggc	ccaggagacg	1260
tggatggcgc	ttcggaccat	catggagcac	accctacta	g		1311

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<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 4

Tyr	His	Asn	Leu	Glu	Glu	Ile	Tyr	Ala	Trp	Leu	Asp	Leu	Leu	Val	Ser	
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Asn	Phe	Pro	Asp	Leu	Val	Ser	Lys	Val	Ser	Ile	Gly	Lys	Ser	Tyr	Glu	
							20			25				30		
Gly	Arg	Asp	Leu	Lys	Val	Leu	Lys	Ile	Ser	Asp	Asn	Pro	Ala	Thr	Gly	
							35			40				45		
Glu	Asn	Glu	Pro	Glu	Val	Phe	Ala	Val	Ala	Gly	Trp	Ile	His	Ala	Arg	
							50			55				60		
Glu	Trp	Val	Thr	Ser	Ala	Thr	Leu	Leu	Trp	Leu	Leu	Lys	Glu	Leu	Val	
							65			70				75		80
Ala	Asn	Tyr	Gly	Ser	Asp	Lys	Thr	Ile	Thr	Lys	Leu	Leu	Asp	Gly	Leu	
							85			90				95		
Asp	Leu	Phe	Tyr	Ile	Leu	Pro	Val	Phe	Asn	Pro	Asp	Gly	Tyr	Ala	Tyr	
							100			105				110		
Ser	Ile	Thr	Thr	Asp	Ser	Tyr	Arg	Met	Trp	Arg	Lys	Thr	Arg	Ser	Pro	
							115			120				125		
Asn	Ala	Gly	Ser	Phe	Cys	Val	Gly	Thr	Asp	Pro	Asn	Arg	Asn	Trp	Tyr	
							130			135				140		
Ala	Gln	Trp	Gly	Gly	Met	Gly	Ala	Ser	Ser	Tyr	Ser	Pro	Cys	Ser	Glu	
							145			150				155		160
Thr	Tyr	Glu	Gly	Thr	Ala	Pro	Phe	Ser	Glu	Pro	Glu	Thr	Lys	Ala	Val	
							165			170				175		
Glu	Asp	Phe	Ile	Arg	Ser	Trp	Leu	Gly	Gly	Lys	Gln	Asn	Ile	Lys		
							180			185				190		
Ala	Tyr	Ile	Thr	Phe	His	Ser	Tyr	Ser	Gln	Leu	Leu	Leu	Tyr	Pro	Tyr	
							195			200				205		
Gly	Tyr	Asp	Tyr	Asn	Leu	Asn	Pro	Asp	Ala	Asn	Asp	Leu	Asp	Glu	Leu	
							210			215				220		
Ser	Asp	Leu	Lys	Ile	Ala	Ala	Asp	Ala	Leu	Ser	Ala	Arg	His	Gly	Thr	
							225			230				235		240
Tyr	Tyr	Thr	Leu	Gly	Leu	Pro	Gly	Ser	Ser	Thr	Ile	Tyr	Pro	Ala	Ser	
							245			250				255		

Ala Gly Gly Ser Asp Asp Trp Ala Tyr Asp Val Gly Ile Ile Lys Tyr
 260 265 270
 Ala Phe Thr Phe Glu Leu Arg Pro Asp Thr Gly Ser Tyr Gly Asn Pro
 275 280 285
 Cys Phe Leu Leu Pro Glu Glu Gln Ile Ile Pro Thr Gly Ser Glu Glu
 290 295 300

<210> 5
 <211> 324
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

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 Tyr His Ser Tyr Glu Glu Ile Asn Ala Trp Leu Asp Asp Leu Ala Arg
 1 5 10 15
 Asn Tyr Pro Asp Leu Thr Ser Val Ser Leu Ile Ser Ile Gly Lys Ser
 20 25 30
 Tyr Glu Gly Arg Pro Ile Lys Val Leu Lys Ile Lys Pro Ala Val Phe
 35 40 45
 Ile Asp Ala Gly Ile His Ala Arg Glu Trp Ile Ala Pro Ala Thr Ala
 50 55 60
 Leu Tyr Leu Ile Asn Gln Leu Leu Thr Asn Glu Thr Glu Tyr Ser Lys
 65 70 75 80
 Asp Pro Asp Asp Glu Gly Ser Val Thr Lys Leu Leu Asp Lys Leu Asp
 85 90 95
 Trp Tyr Ile Val Pro Val Met Asn Pro Asp Gly Tyr Glu Tyr Thr His
 100 105 110
 Thr Ser Thr Asp Arg Leu Trp Arg Lys Asn Arg Ser Pro Asn Gly Ala
 115 120 125
 Ser Gly Ser Gln Gly Thr Trp Tyr Asn Cys Tyr Gly Val Asp Leu Asn
 130 135 140
 Arg Asn Phe Asp Phe His Asn Trp Gly Glu Ile Gly Ser Ser Ser
 145 150 155 160
 Leu Pro Cys Ser Glu Thr Tyr Ala Gly Ser Ser Pro Phe Ser Glu Trp
 165 170 175
 Glu Pro Glu Thr Lys Ala Leu Leu Asp Phe Ile Leu Ser Asn Glu Ile
 180 185 190
 Gly Lys Gly Arg Ile Lys Ala Tyr Ile Ser Leu His Ser Tyr Ser Gln
 195 200 205
 Leu Leu Leu Tyr Pro Tyr Gly Tyr Thr Asn Ala Thr Val Pro Pro Asn
 210 215 220
 Gly Glu Asp Leu His Lys Glu Val Ala Lys Ala Ala Ala Lys Ala Ile
 225 230 235 240
 Gly Asp Tyr Tyr Phe Gly Gly Thr Leu Tyr Thr Pro Gly Ser Ser Ser
 245 250 255
 Ala Asp Pro Asp Leu Asp Ile Thr Leu Tyr Pro Ala Ser Gly Gly Ser
 260 265 270
 Asp Asp Trp Ala Tyr Gly Thr Leu Lys Gly Val Lys Tyr Ser Tyr Thr
 275 280 285
 Ile Glu Leu Arg Asp Thr Gly Asp Asp Ala Gly Arg Tyr Gly Phe Leu
 290 295 300
 Leu Pro Pro Ser Cys Val Lys Pro Val Arg Met Glu Gln Ile Ile Pro
 305 310 315 320
 Thr Gly Glu Glu

<210> 6
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

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Lys Asp Leu Glu Asn Thr Glu His Leu Glu Leu Asp Phe Trp Lys Pro
20 25 30
Asp Ser Ala Thr Pro Ile Lys Pro Gly Ser Thr Val Asp Phe Arg Val
35 40 45
Pro Ala Glu Asp Ile Gln Ala Val Lys Ser Phe Leu Glu Gln Ser Gly
50 55 60
Ile His Tyr Glu Val Leu Ile Glu Asp Val Gln Glu Leu Leu Glu Glu
65 70 75 80
Gln Phe